



SEQUENCE LISTING

<110> Sauter, Margret M
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
CONDITIONS

<130> 2283/201

<140> 09/785,738

<141> 2001-02-16

<150> 60/183,572

<151> 2000-02-18

<160> 18

<170> PatentIn Ver. 2.1

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<211> 872

<212> DNA

<213> Rice

<220>

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<222> (69)..(668)

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Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
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cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
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gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
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ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
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Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
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Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
130 135 140

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Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
145 150 155

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Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
160 165 170

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His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
175 180 185 190

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Gly Glu Asn Gln Ala Val Glu Gly Phe
195 200

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ggctatgggc gccactcacc aacttgaagt gaaagatttta atgattttttg ttaattctta 808

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35 40 45
Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
50 55 60
Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
85 90 95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Ile
115 120 125
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130 135 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
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 gtctgagagg ttccagag atg gag aac cag ttc cag gat ggc aag gag gag 171
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 gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
 Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
 15 20 25
 cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
 Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
 30 35 40
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 Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
 45 50 55
 gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
 Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
 60 65 70 75
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 Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
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 ctg aaa aat ttc ttt gaa gaa cac ttg cat act gat gaa gag ata cgc 459
 Leu Lys Asn Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg
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 Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp
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 cag tgg atc cgt gta gca gtg aag aaa ggg gcc atg att gtt ttg cct 555
 Gln Trp Ile Arg Val Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro
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 gcg gga atg tat cac cgc ttc aca ttg gac agt gac aac tac atc aag 603
 Ala Gly Met Tyr His Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys
 140 145 150 155

gca atg cgg ctc ttt gtg gga gag cct gtc tgg acg ccg tac aac cgt 651
Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg
160 165 170

ccc cat gac cat ctg cca gct aga aag gag tat gtc gaa aaa att atc 699
Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Val Glu Lys Ile Ile
175 180 185

aac agg ggt gga act caa gct gtc gaa gct cgt taa aggcataatca 745
Asn Arg Gly Gly Thr Gln Ala Val Glu Ala Arg
190 195

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tcagctgttg caatgggctc ctaccgacat cttacatcat ttggcagtat ttgacacaaa 865

cccgcttaaa atctccctga aaatacgcac gtcacatgt cagagtgttt atatacaata 925

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35 40 45
Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn Asp Glu Asn Leu Lys
50 55 60
Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met Asp Ile Cys Asp Val
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Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys Leu Lys Asn Phe Phe
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Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu Glu Gly
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Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile Arg Val
115 120 125
Ala Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met Tyr His
130 135 140
Arg Phe Thr Leu Asp Ser Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
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gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt	144
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu	
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Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu	
50 55 60	
gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa	240
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys	
65 70 75 80	
cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg	288
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu	
85 90 95	
cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt	336
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe	
100 105 110	
gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa	384
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys	
115 120 125	
ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt	432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu	
130 135 140	
gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca	480
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro	
145 150 155 160	
att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa	528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln	
165 170 175	
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Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val	
180 185 190	
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Asn Ala Ala Ala	
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aataaatatt accatatggt ggctttgctg ttcttgatgt gtgccttact aagcatgttt	691
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gat	cag	cgg	cta	ccg	cac	cag	aag	aac	cca	ccg	gag	ttt	gtt	tca	gtg		95	
Asp	Gln	Arg	Leu	Pro	His	Gln	Lys	Asn	Pro	Pro	Glu	Phe	Val	Ser	Val			
				20					25					30				
gag	aaa	tta	gca	gta	atc	gga	gtt	tta	tac	tgg	aaa	ttg	aac	cct	aat		143	
Glu	Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn			
			35					40					45					
gat	tac	gag	aac	gat	gaa	gaa	ttg	aaa	aaa	att	cgt	caa	agt	aga	ggc		191	

Asp Tyr	Glu Asn	Asp Glu	Glu Leu	Lys Lys	Ile Arg	Gln Ser	Arg Gly		
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tac agc	tac atg	gac ttg	ctg gat	ttg tgc	cct gag	aag gtg	gat aac	239	
Tyr Ser	Tyr Met	Asp Leu	Leu Asp	Leu Cys	Pro Glu	Lys Val	Asp Asn		
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tat gag	cag aag	ttg aaa	aat ttc	tat acg	gag cac	ata cac	gca gat	287	
Tyr Glu	Gln Lys	Leu Lys	Asn Phe	Tyr Thr	Glu His	Ile His	Ala Asp		
80		85			90		95		
gag gag	ata cgt	tac tgt	ctg gaa	ggg agt	gga tat	ttt gat	gtg aga	335	
Glu Glu	Ile Arg	Tyr Cys	Leu Glu	Gly Ser	Gly Tyr	Phe Asp	Val Arg		
	100			105		110			
gac aag	gat gat	cgc tgg	att cgc	atc tgg	atg aag	gcc ggt	gat atg	383	
Asp Lys	Asp Asp	Arg Trp	Ile Arg	Ile Trp	Met Lys	Ala Gly	Asp Met		
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att gtc	ttg cct	gct ggg	att tac	cac cgg	ttc acc	cta gat	act gat	431	
Ile Val	Leu Pro	Ala Gly	Ile Tyr	His Arg	Phe Thr	Leu Asp	Thr Asp		
	130		135			140			
aac tat	gtc aag	ttg atg	agg ttg	ttt gtg	gga gag	cgg gtg	tgg acg	479	
Asn Tyr	Val Lys	Leu Met	Arg Leu	Phe Val	Gly Glu	Pro Val	Trp Thr		
145			150		155				
cct tac	aat cga	cca caa	gaa gat	cat cca	gca agg	aag gag	tac atc	527	
Pro Tyr	Asn Arg	Pro Gln	Glu Asp	His Pro	Ala Arg	Lys Glu	Tyr Ile		
160		165			170		175		
aag agt	gtt act	gaa aga	gta gga	gtg cct	ctt aca	gca cac	taa	572	
Lys Ser	Val Thr	Glu Arg	Val Gly	Val Pro	Leu Thr	Ala His			
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 Lys Leu Ala Val Ile Gly Val Leu Tyr Trp Lys Leu Asn Pro Asn Asp
 35 40 45
 Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Gln Ser Arg Gly Tyr
 50 55 60
 Ser Tyr Met Asp Leu Leu Asp Leu Cys Pro Glu Lys Val Asp Asn Tyr
 65 70 75 80
 Glu Gln Lys Leu Lys Asn Phe Tyr Thr Glu His Ile His Ala Asp Glu
 85 90 95
 Glu Ile Arg Tyr Cys Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp
 100 105 110
 Lys Asp Asp Arg Trp Ile Arg Ile Trp Met Lys Ala Gly Asp Met Ile
 115 120 125
 Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp Asn

400> 9																	
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Pro	Arg	Glu	Asp	Val	Leu	Gln	Ala	Trp	Tyr	Met	Asp	Asp	Ser	Asp	Glu		
								15					20				
gat	caa	aga	ctc	ccc	cac	cac	aaa	gaa	ccc	aag	gag	ttt	gtc	tcg	ttg		148
Asp	Gln	Arg	Leu	Pro	His	His	Lys	Glu	Pro	Lys	Glu	Phe	Val	Ser	Leu		
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gac	caa	ctt	gct	gaa	ctt	gga	gtc	ctt	agc	tgg	aaa	cta	gat	gct	gat		196
Asp	Gln	Leu	Ala	Glu	Leu	Gly	Val	Leu	Ser	Trp	Lys	Leu	Asp	Ala	Asp		
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aac	cat	gaa	aat	gat	cca	gag	ctg	aag	aag	att	cgt	gaa	gag	cgt	ggg		244
Asn	His	Glu	Asn	Asp	Pro	Glu	Leu	Lys	Lys	Ile	Arg	Glu	Glu	Arg	Gly		
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tac	acc	tac	atg	gat	gtt	tgt	gag	gtc	tgc	cca	gaa	aag	tgt	cca	aat		292
Tyr	Thr	Tyr	Met	Asp	Val	Cys	Glu	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn		
tat	gaa	cag	aaa	atc	aaa	agc	ttc	ttt	gaa	gag	cat	ctt	cac	act	gat		340
Tyr	Glu	Gln	Lys	Ile	Lys	Ser	Phe	Phe	Glu	Glu	His	Leu	His	Thr	Asp		
gag	gag	atc	cgc	ttt	tgt	gct	gct	gga	agt	ggc	tat	ttt	gat	gtt	agg		388
Glu	Glu	Ile	Arg	Phe	Cys	Ala	Ala	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg		
gat	cgc	aat	gaa	gct	tgg	att	cgt	gtg	tgg	gtc	aag	aaa	gga	gga	atg		436
Asp	Arg	Asn	Glu	Ala	Trp	Ile	Arg	Val	Trp	Val	Lys	Lys	Gly	Gly	Met		
atc	atc	tta	cct	gcc	gga	att	tat	cat	cgc	ttt	acg	cta	gat	gag	agc		484
Ile	Ile	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Glu	Ser		
aac	tac	att	aag	gct	ttg	cgt	ttt	ttt	ggt	qag	cca	gtt	tgg	act			532


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Pro Tyr Asn Arg Pro Asn Asp His Leu Pro Ala Arg Gln Gln Tyr Val
    170                                175                                180

aag gat ttt gtg gaa aag gat gtt agc agc cat gct gtt gat gcc acc    628
Lys Asp Phe Val Glu Lys Asp Val Ser Ser His Ala Val Asp Ala Thr
    185                                190                                195

gcg taa gatctggttc tgccaatca tagtaccaca tgaaaaggac caagactttg    684
Ala
200

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Pro Lys Glu Phe Val Ser Leu Asp Gln Leu Ala Glu Leu Gly Val Leu
          35          40          45
Ser Trp Lys Leu Asp Ala Asp Asn His Glu Asn Asp Pro Glu Leu Lys
          50          55          60
Lys Ile Arg Glu Glu Arg Gly Tyr Thr Tyr Met Asp Val Cys Glu Val
          65          70          75          80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Gln Lys Ile Lys Ser Phe Phe
          85          90          95
Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Phe Cys Ala Ala Gly
          100          105          110
Ser Gly Tyr Phe Asp Val Arg Asp Arg Asn Glu Ala Trp Ile Arg Val
          115          120          125
Trp Val Lys Lys Gly Gly Met Ile Ile Leu Pro Ala Gly Ile Tyr His
          130          135          140
Arg Phe Thr Leu Asp Glu Ser Asn Tyr Ile Lys Ala Leu Arg Phe Phe
          145          150          155          160
Val Gly Glu Pro Val Trp Thr Pro Tyr Asn Arg Pro Asn Asp His Leu
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Pro Ala Arg Gln Gln Tyr Val Lys Asp Phe Val Glu Lys Asp Val Ser
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Ser His Ala Val Asp Ala Thr Ala
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<222> (33)..(635)

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Lys Arg Glu Glu Val Ile Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
10 15 20

gat cag agg ctt cct cat cac cgt gaa cct aag gaa tat gta tcc ttg 149
Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Tyr Val Ser Leu
25 30 35

gat aaa ctt gct gag ctt gga gta ctc agc tgg cga ttg gat gct gat 197
Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu Asp Ala Asp
40 45 50 55

aac tat gaa aat gat gaa gag ttg aag aaa att cgt gaa gaa cga ggt 245
Asn Tyr Glu Asn Asp Glu Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
60 65 70

tac tcc tac atg gac ttc tgc gag gtt tgc cct gag aag ctt cca aat 293
Tyr Ser Tyr Met Asp Phe Cys Glu Val Cys Pro Glu Lys Leu Pro Asn
75 80 85

tat gag gag aag ata aaa aat ttc ttc gaa gaa cat att cat act gat 341
Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Ile His Thr Asp
90 95 100

gag gag atc cgt tac tgt gtg gca gga agt ggt tat ttt gat gta cgg 389
Glu Glu Ile Arg Tyr Cys Val Ala Gly Ser Gly Tyr Phe Asp Val Arg
105 110 115

gat cat aat gat aaa tgg att cgt gtg tgg gtg aag aaa gga ggc atg 437
Asp His Asn Asp Lys Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120 125 130 135

ata gtt tta cct gct gga att tat cat cgc ttt act ctg gat aca gac 485
Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Thr Asp
140 145 150

aac tat att aag gca atg cgg ctc ttt gtt ggt gat cca att tgg act 533
Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro Ile Trp Thr
155 160 165

cgg tac aat cgt cgg cac gat cat ctt cct gca agg aag gag tat atc 581
Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
170 175 180

aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
185 190 195

gca taa aatcaacatt catctgggtgg tggccaagtc gttgatgctg cgcataaaa 685
Ala
200

tcagcattca tctctgggtat cgtgtcttat aaaatatgaa accccggatt tgtggaata 745
aataagtcta ggcttgctg cttttgatgc gtggatatgg atcggtatgg ttgttgcttg 805
ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtattt ctacatttta 865
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35 40 45
Ser Trp Arg Leu Asp Ala Asp Asn Tyr Glu Asn Asp Glu Glu Leu Lys
50 55 60
Lys Ile Arg Glu Glu Arg Gly Tyr Ser Tyr Met Asp Phe Cys Glu Val
65 70 75 80
Cys Pro Glu Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe
85 90 95
Glu Glu His Ile His Thr Asp Glu Glu Ile Arg Tyr Cys Val Ala Gly
100 105 110
Ser Gly Tyr Phe Asp Val Arg Asp His Asn Asp Lys Trp Ile Arg Val
115 120 125
Trp Val Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His
130 135 140
Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg Leu Phe
145 150 155 160
Val Gly Asp Pro Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu
165 170 175
Pro Ala Arg Lys Glu Tyr Ile Lys Asn Phe Leu Arg Glu Glu Gly Gly
180 185 190
Gly Gln Ala Val Asp Ala Ala Ala
195 200

<210> 13
<211> 920
<212> DNA
<213> Human

<220>
<221> CDS
<222> (1) .. (564)

<400> 13

cga aca cgg cac ccg cac tgc gcg tca gtg gtg cag gcc tgg tat atg 48
 Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
 1 5 10 15

gac gac gcc ccg ggc acc cgc ggc aac ccc acc gcc ccg acc ccg gcc 96
 Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
 20 25 30

gcc cag tgc gct gga gca gct gcg cgg ctc ggg gtg ctc tac tgg aag 144
 Ala Gln Cys Ala Gly Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
 35 40 45

ctg gat gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga 192
 Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
 50 55 60

aga gag agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat 240
 Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Thr Ile Cys Lys Asp
 65 70 75 80

aaa cta cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat 288
 Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
 85 90 95

ttg cac ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac 336
 Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
 100 105 110

ttc gat gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag 384
 Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
 115 120 125

aag gga gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg 432
 Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
 130 135 140

gtg gac gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa 480
 Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
 145 150 155 160

ccg gtg tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc 528
 Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
 165 170 175

ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgtgcc 574
 Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
 180 185

tgggaaactaa cacgtgcctc gttaaaggctc ccaatgtaat gaactgagca gaaaattcaa 634

tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694

ttatttgatc agaattttt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga 754

gtcaccttca ttttctgtaa ctcaatcaag actggtgggt ccatggccct gtgttagttc 814

attgcattca ggttgagtc caaatgaaag tttcatctcc cgaatgcag ttccttagat 874

gcccactctg acgtgaatgc cgcgcctcgt tgtaagaagg tgcaat 920

<210> 14
<211> 187
<212> PRT
<213> Human

<400> 14
Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
1 5 10 15
Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
20 25 30
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
35 40 45
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
50 55 60
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
65 70 75 80
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
85 90 95
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
100 105 110
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
115 120 125
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
130 135 140
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
145 150 155 160
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
165 170 175
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

<210> 15
<211> 972
<212> DNA
<213> Mouse

<220>
<221> CDS
<222> (17) .. (556)

<400> 15
agccgccgcc gccacc atg gtg cag gcc tgg tat atg gac gag tcc acc gcc 52
Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
1 5 10
gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg 100
Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
15 20 25
gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148
Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
30 35 40
aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196
Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
45 50 55 60
tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244
Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn

	65	70	75	
tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat				292
Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp				
	80	85	90	
gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg				340
Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg				
	95	100	105	
gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg				388
Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met				
	110	115	120	
att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag				436
Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys				
	125	130	135	140
aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca				484
Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr				
	145	150	155	
cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg				532
Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met				
	160	165	170	
agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt				586
Ser Phe Leu Glu Gly Thr Ala				
	175	180		
gtgaatctcc tgctgtgga accgaatgga aagtgtctca cttttctgct tttgtatttg				646
aacttgaggc tagactagct ctctttgcta ggattgtgag atcagtgtct tttaaatgaa				706
agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat				766
tttccttaac tgtaagact tagaggtata ggagccctgg attggtatgt gcattcatgc				826
atggccaatc ttcatctccc agatcttttag gtgtctgttg gtgtgaagct atgcctcctg				886
caagagggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg				946
ttgagtgggg aagtgggggtt gttggtt				972

<210> 16
 <211> 179
 <212> PRT
 <213> Mouse

<400> 16
 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala Asp Pro Arg Lys
 1 5 10 15
 Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu Glu Gln Leu Arg
 20 25 30
 Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn
 35 40 45
 Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn Tyr Ser Trp Met
 50 55 60
 Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn Tyr Glu Glu Lys
 65 70 75 80

Ile	Lys	Met	Phe	Phe	Glu	Glu	His	Leu	His	Leu	Asp	Glu	Glu	Ile	Arg
				85					90					95	
Tyr	Ile	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp
			100					105					110		
Lys	Trp	Ile	Arg	Ile	Ser	Met	Glu	Lys	Gly	Asp	Met	Ile	Thr	Leu	Pro
		115					120					125			
Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Glu	Lys	Asn	Tyr	Val	Lys
	130					135					140				
Ala	Met	Arg	Leu	Phe	Val	Gly	Glu	Pro	Val	Trp	Thr	Pro	Tyr	Asn	Arg
	145				150				155					160	
Pro	Ala	Asp	His	Phe	Asp	Ala	Arg	Val	Gln	Tyr	Met	Ser	Phe	Leu	Glu
				165				170						175	
Gly	Thr	Ala													

<210> 17

<211> 706

<212> DNA

<213> Zebrafish

<220>

<221> CDS

<222> (36)..(581)

<223> n at positions 634 and 642 is unknown

<400> 17

gtactgcgca	tgagaccca	accggactgt	tcaag	atg	agt	gtt	ttc	gag	gca	53
					Met	Ser	Val	Phe	Glu	Ala
					1				5	

tgg	tac	atg	gat	gaa	gag	tcc	gga	gag	gac	cag	aga	ctc	ccg	cac	aaa	101
Trp	Tyr	Met	Asp	Glu	Glu	Ser	Gly	Glu	Asp	Gln	Arg	Leu	Pro	His	Lys	
			10					15					20			

ctg	agc	ccg	aat	cag	ccc	gtc	agc	gtc	cag	cag	ctg	gag	cac	atc	gga	149
Leu	Ser	Pro	Asn	Gln	Pro	Val	Ser	Val	Gln	Gln	Leu	Glu	His	Ile	Gly	
		25				30						35				

gtc	ttt	cac	tgg	aag	ctg	aac	gct	gat	atc	tat	gaa	aat	gac	ccc	gaa	197
Val	Phe	His	Trp	Lys	Leu	Asn	Ala	Asp	Ile	Tyr	Glu	Asn	Asp	Pro	Glu	
	40					45					50					

ctg	cag	aag	atc	cga	gag	gag	aag	ggc	tat	tcc	ttt	atg	gac	atc	ata	245
Leu	Gln	Lys	Ile	Arg	Glu	Glu	Lys	Gly	Tyr	Ser	Phe	Met	Asp	Ile	Ile	
	55				60				65					70		

acc	att	cac	ccg	gac	aaa	ctg	ccc	gat	tac	caa	aac	aaa	ctg	aaa	atg	293
Thr	Ile	His	Pro	Asp	Lys	Leu	Pro	Asp	Tyr	Gln	Asn	Lys	Leu	Lys	Met	
			75						80					85		

ttt	tac	gaa	gag	cat	ctc	cac	ctg	gac	gat	gag	atc	cgt	tat	att	ctg	341
Phe	Tyr	Glu	Glu	His	Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	
		90					95						100			

gaa	gga	tcc	tct	tat	ttt	gat	gtg	cgg	gac	gaa	ggc	gac	cgc	tgg	atc	389
Glu	Gly	Ser	Ser	Tyr	Phe	Asp	Val	Arg	Asp	Glu	Gly	Asp	Arg	Trp	Ile	
		105					110					115				

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cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att 437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
    120                125                130

tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt 485
Tyr His Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
    135                140                145                150

ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat 533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
    155                160                165

gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga 581
Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
    170                175                180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct tanacagaca 641
ngcagcaata gttagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701
attat 706

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<210> 18
 <211> 181
 <212> PRT
 <213> Zebrafish
 <223> n at positions 634 and 642 is unknown

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<400> 18
Met Ser Val Phe Glu Ala Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp
  1          5          10          15
Gln Arg Leu Pro His Lys Leu Ser Pro Asn Gln Pro Val Ser Val Gln
    20          25          30
Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
    35          40          45
Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
    50          55          60
Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
    65          70          75          80
Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
    85          90          95
Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
    100          105          110
Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
    115          120          125
Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
    130          135          140
Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
    145          150          155          160
Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
    165          170          175
Ser Leu Gly Ser Ser
    180

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